I claim:

1. A method for interfering with the expression of hyphal-specific genes in a fungus resulting in the inhibition of cell growth of said fungus, comprising the step of:

interfering with the transcription of said hyphal-specific genes mediated by *cis* acting sequences.

2. The method of claim 1, wherein said fungus comprises a pathogenic or nonpathogenic yeast strain.

3. The method of claim 2, wherein said pathogenic fungus comprises *Candida albicans*.

4. The method of claim 1, wherein said *cis* acting sequences comprise *cis*-regulatory elements.

5. The method of claim 4, wherein said *cis*-regulatory elements comprise UAS.

6. The method of claim 4, wherein said *cis*-regulatory elements comprise URS.

7. The method of claim 4, wherein said interfering step comprises interfering with DNA BP that bind to said *cis*-regulatory elements.

8. The method of claim 7, wherein said interfering step comprises interfering with regulatory proteins specific to said DNA BP.

9. The method of claim 1, wherein said interfering step comprises manipulating environmental factors.

10. The method of claim 1, wherein said interfering step comprises manipulating signal transduction pathways.

11. The method of claim 7, wherein said interfering with DNA BP comprises manipulating the binding of said DNA BP to said *cis* regulatory elements.

12. The method of claim 7, wherein interfering with DNA BP comprises manipulating the expression of said DNA BP.

13. The method of claim 8, wherein interfering with DNA BP regulatory proteins comprises manipulating the ability of said DNA BP regulatory proteins to bind to said DNA BP.

14. The method of claim 8, wherein said interfering with DNA BP regulatory proteins comprises manipulating the expression of said DNA BP regulatory protein.

15. The method of claim 9, wherein said manipulating environmental factors comprises changing the environmental temperature of said fungus.

16. The method of claim 9, wherein said manipulating environmental factor comprises modifying the nitrogen available to said fungus.

17. The method of claim 9, wherein said interfering with environmental factor comprises altering the level of nitrogen available to said fungus.

18. The method of claim 1, wherein said hyphal-specific genes are selected from the group consisting of HYR1, ECE1, ALS3, CHS2, and SAP6.

19. The method of claim 1, wherein said hyphal-specific gene comprises HWP1.

20. The method of claim 19, wherein said HWP1 gene contains said *cis* acting sequences within its promoter region.

21. The method of claim 20, wherein said HWP1 promoter region comprises the following isolated DNA sequence [SEQ. ID. NO:1]:
GGATCTTTCTTTTTCATTTCCCTTAAAACCGATCAAGAAAGAAAGTGGAAATAAA
GCTATGATAAATGTTGATTTTGTGTAATTCAATCAACTAAGCACGTTTGACAGTT

AAAAAGTACGTTGTTGTTGTCCTCGTCTCGTCTAATTTCTGTTGACGAGGATTAAT
AACAAGAAATACAGGAAACCCTCCAAAAAAAAAAATTTTGGACCTTACACGCACA
TAAATTGCGGATAAACTTGCCATAATAAAAACTCTTTGAAACATACGATATGTTA
TTCTTTTCATAACTGGAATATTTTTGCTTTTTTTTAACATTATGAACAATTGAAAA
AAAAAGGAAATGAAAAGGTAAGAGTTGCCTAACCATTGAAAATAATAGGCTAAG
GTTTTTCCTGATGCGTTTAACTAAAAAGGAAATAACAAAAGTTATTAGCGATAAC
CTGCGTAAGGTGTCAACAAAATATATTTTGCACGTTAGCTCTATAGAAAATATAC
AAACTAAATCCTTAAGGAATTTCCTCTATATATAATAGGAAATCCCTCTCACAGT
GAACTGAATTATCCATCTGAATTATCAGTCCACTAATTCCATCAATAAAATAGAT
TAGTGTATTGTTCTCTTCAGTACAATTACTACCATTATGCAATGCTAGCTTATTGT
TCATAATTAGCCATGTTGCACACCCTAATTCGAACATTAACTGTATCCATATTTTT
CTTGTCCTTCTTTGTTTTTTTCTAACAAAAATGTTCCAGAATTTTTTAAAAAATATT
TGAAAAAACACATAACACTTTGAGTATGATAATATCAACTATTGACTTGTTTTGA
AAGTAAAGAATCAAATTTTTTTCTAACTCGACTAATGCACTTTACATCAACTGGA
TGTTATTTGCATCTACTACTATAAGCTCAAACAAATTATCTTTCAAAAATGTTATA
ATTAACAAGTCATCTATAATTCTTTGGATCCAAAAACAAGGAATTCGGAAATTCT
GACGATAAATGTCGACTCACAATTCATTGTAAAAAGGGAGAGTTTTGGTAGGCTC
ATAATCGCTTATAATGTACCTCTAAAGTAATCTAAAACAAACACAACCTTTCTAA
AACCTATAATAATAACCCTAATGGCTCACAACCGGGATAATGTTAGTTAGCCCAG
CTGTTTTTTTTTTGCCTTATTTTTATGACTACATTTTGTTTCACTTTTTGTTGCGACT
TTAATACCGTTTTTGCAACTTCTCTTTGTATCACCTGTATCCGCCTTTTTTAACATA
GCAACTCTTGTAAAGTCCCTTTCTTTTCCCACTATTTTATCATTCTTGAAATATGT
AATCAGAATAGTTTTTCAAAAACTATAAATAACGGTCAAAATAACCGGCTATTTT
CAATTTCCATTCAACTTGTTTTCTCAACAATATCAAACACAACAGGAATCTCCTAT
AGTCACTCGCTTTTAGTTTCGTCAATATG;

including any insertions, deletions, mutations, or modifications.

22. The method of claim 1, wherein said cell growth inhibition is in a patient.

23. The method of claim 22, wherein said patient is afflicted with a disease.

24. The method of claim 23, wherein said disease is AIDS.

25. The method of claim 22, wherein said patient is immunocompromised.

26. The method of claim 22, wherein said patient is an organ transplant recipient.

27. The method of claim 1, wherein said hyphal-specific genes comprise genes responsible for controlling dimorphism.

28. The method of claim 4, wherein said *cis*-regulatory elements comprise a NIT2 binding site.

29. The method of claim 7, wherein said DNA BP is encoded by a nucleotide sequence for the DNA binding domain that is homologous to a nucleotide sequence encoding the DNA binding domain of NIT2 binding proteins.

30. The method of claim 29, wherein the DNA BP is selected from the group consisting of GAT99, GAT-1, or GATA-like binding proteins.

31. The method of claim 29, wherein said NIT2 DNA binding domain comprises the protein sequence [SEQ. ID. NO: 2]:
CTNCFTQTTPLWRRNPDGQPLCNACGLFLKLHGVVRPLSLKTDVIKKRNR.

32. The method of claim 29, wherein the DNA binding domain of said DNA BP comprises the protein sequence [SEQ. ID. NO: 3]:
CTNCGTKTTPLWRRNPQGQPLCNACGLFLKLHGVVRPLSLKTDVIKKRQR.

33. The method of claim 10, wherein said signal transduction pathways comprises a cAMP-dependent signaling pathway.

34. The method of claim 1, wherein said interfering step inhibits transcription of genes essential for adhesion of said fungus to a patient.

35. A method for characterizing genes under control of DNA BP in fungus comprising the steps of:

creating a genomic DNA library from a fungus;
screening said genomic library with cDNA from fungal strains;
sequencing the clones of interest from said screening step.

36. The method of claim 35, wherein said fungus is a pathogenic or nonpathogenic yeast strain.

37. The method of claim 36, wherein said pathogenic yeast strain is *Candida albicans*.

38. The method of claim 35, wherein said genomic library is a *Candida albican*s genomic DNA library.

39. The method of claim 35, wherein said creating step further comprises the steps of:

digesting genomic DNA with a restriction enzyme;
selecting genomic fragments ranging in size from 0.5 to 2.0 Kb; and
cloning said genomic fragments into a plasmid vector.

40. The method of claim 35, wherein said screening step further comprises the steps of:

transferring said cloned genomic fragments onto 96-well plates;
performing colony PCR using universal primers;
checking said PCR reactions on gels and rearray positives on 96-well plates;
spotting productive PCR reactions on membranes;
preparing and labeling cDNA from mRNA of fungal strains;
hybridizing labeled cDNA to duplicate membranes; and
isolating the clones of interest.

41. The method of claim 40, wherein said fungal strains contain or do not contain DNA BP genes.

42. An isolated, purified nucleic acid sequence comprising a nucleic acid sequence encoding *C. albicans* 5' flanking region [SEQ. ID. NO:1].

43. An isolated purified nucleic acid sequence comprising a nucleic acid seqeunce encoding *C. albicans* 3' flanking sequence [SEQ. ID. NO: 4].